

Multiancestry genome-wide association and multiomics analyses elucidate spatiocellular features of multiple sclerosis genetics

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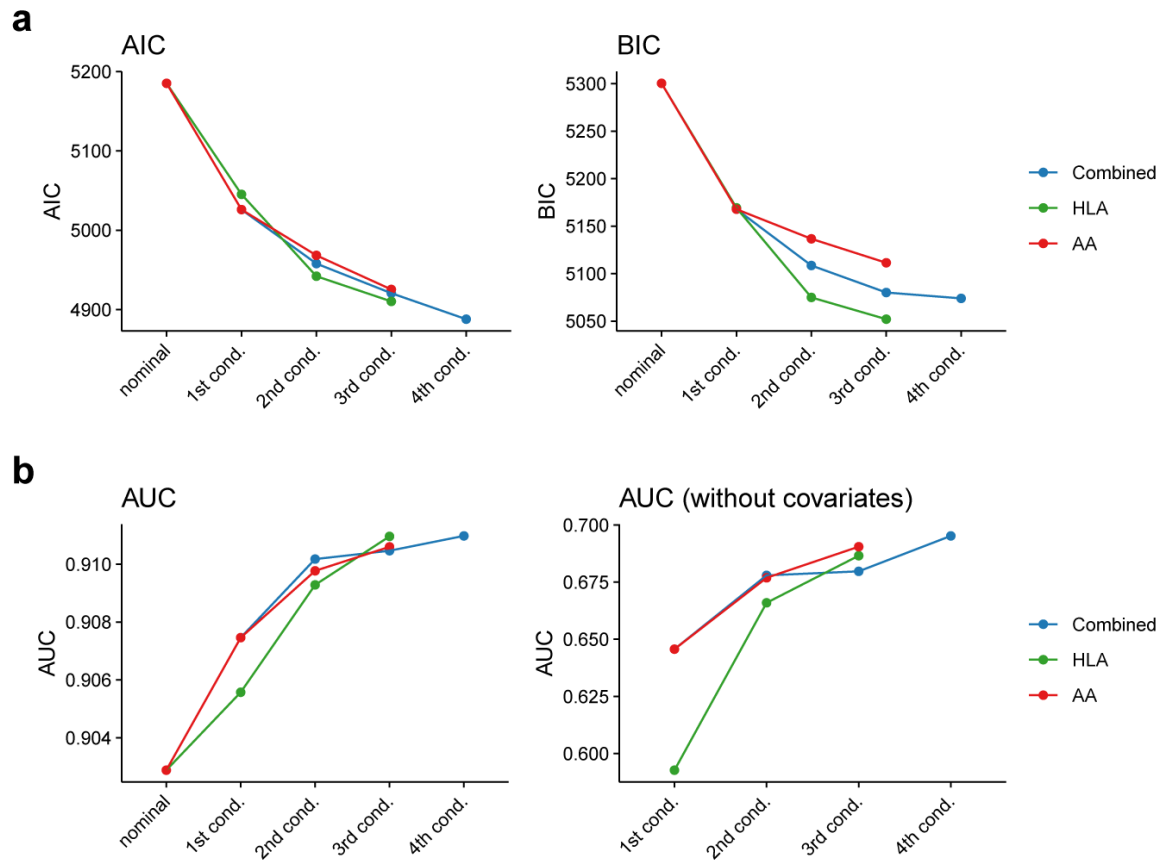
Supplementary Figures

Supplementary Fig. 1: Comparison of HLA fine-mapping models across conditional steps.

Supplementary Fig. 2: scDRS results for AIDA PBMC scRNA-seq.

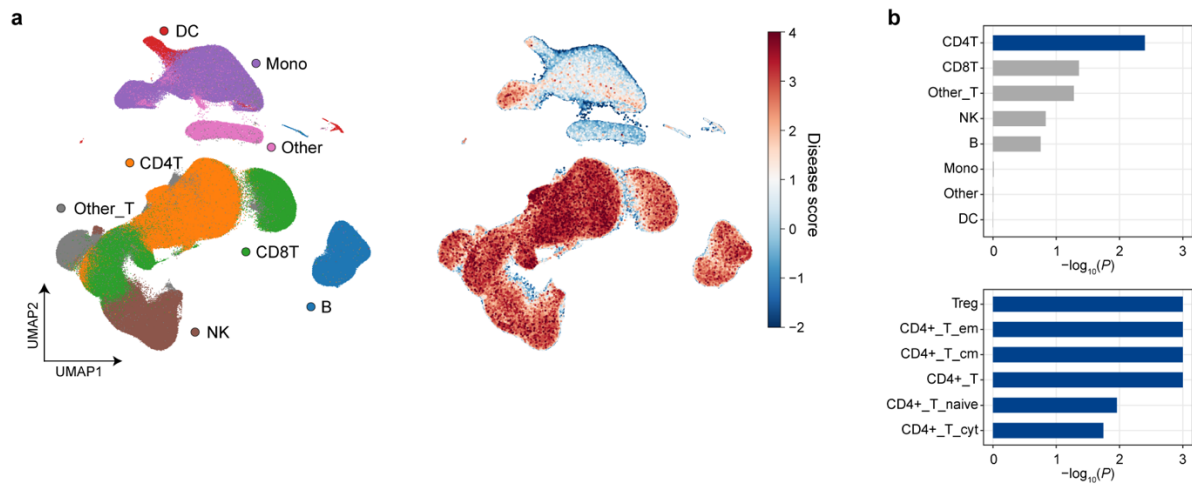
Supplementary Fig. 3: scDRS results for MS subcortical lesion snRNA-seq excluding immune cells.

Supplementary figure 4: Sensitivity analysis of scDRS using different numbers of MAGMA genes.



Supplementary Fig. 1: Comparison of HLA fine-mapping models across conditional steps.

(a) AIC and BIC values across conditional steps. (b) AUC from 10-fold cross-validation, shown for models with covariates (left) and without covariates (right). AIC, Akaike's information criterion; BIC, Bayesian information criterion; AUC, area under the receiver operating characteristic curve.



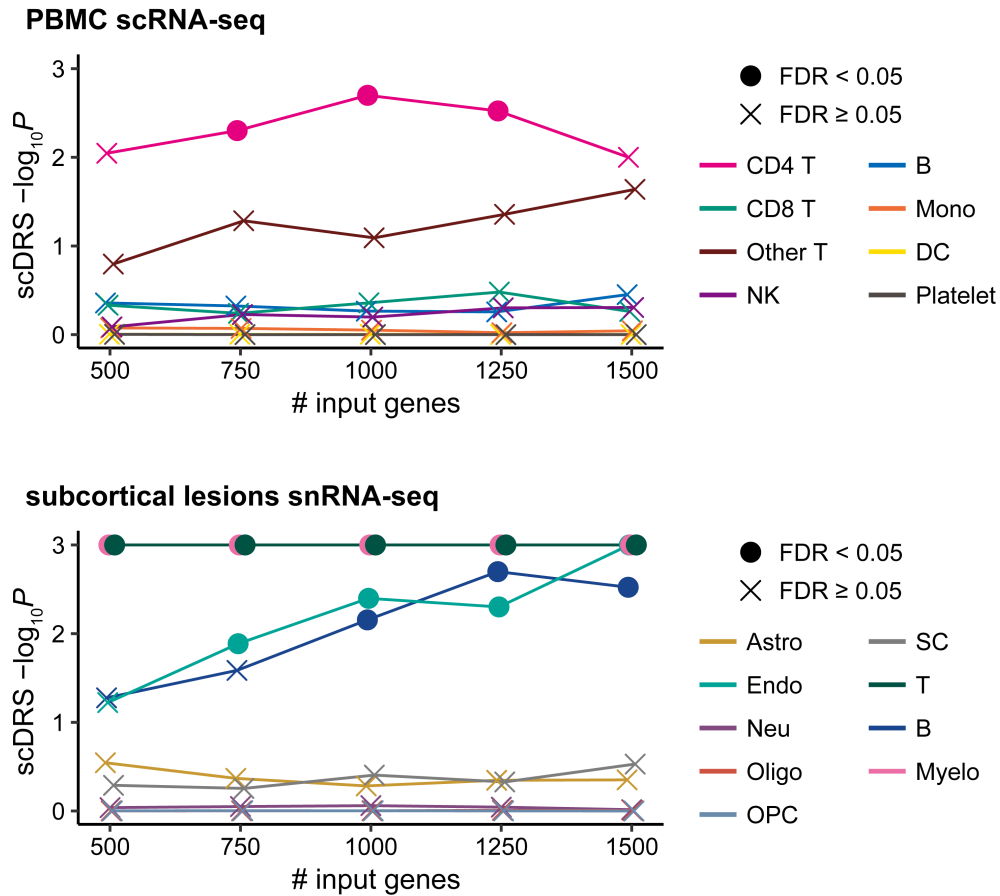
Supplementary Fig. 2: scDRS results for AIDA PBMC scRNA-seq.

(a) UMAP of the AIDA PBMC scRNA-seq excluding immune cells colored by the main cell types (left) and by the scDRS disease score (right). (b) Bar plots of the association of the main cell types (top) and the sub-cell types of CD4+ T cells (bottom) for MS. Unadjusted P -values are shown on the x-axis, and bars colored in deep blue denote significant cell type-disease associations (FDR < 0.05). FDR was calculated via the Benjamini–Hochberg method across cell types.



Supplementary Fig. 3: scDRS results for MS subcortical lesion snRNA-seq excluding immune cells.

(a) UMAP of the MS subcortical lesion snRNA-seq excluding immune cells colored by the main cell types (left) and by the scDRS disease score (right). (b) Bar plots showing the association of the brain cell types for MS. Unadjusted P -values are shown on the x-axis, and bars colored in deep blue denote significant cell type-disease associations (FDR < 0.05). FDR was calculated via the Benjamini–Hochberg method across cell types.



Supplementary figure 4: Sensitivity analysis of scDRS using different numbers of MAGMA genes.

The x-axis indicates the number of input genes for scDRS, and the y-axis indicates the scDRS $-\log_{10}P$ for each cell type.